

FIGURE 1

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HKLK2.LA0	(6998)	AA-CTGAGCCTTGATTATATTG-GAGCTTGGTTGCA-CAG-ACATGTGGA
PSE	(589)	AATCT-AG-C-TGA-TATAGTGTG-GCTCAAAACCTTCAGCACAAATC-A
HKLK2.LA0	(7044)	CCACCTTCATGGCTGAACCTTAGTACTTAGCCCCCTCCAGACGTCTACAGC
PSE	(553)	-CACCGTTA-GACT--A-TCTGGT--GT-G--GC-CCAAAC--CTTCAGG
HKLK2.LA0	(7094)	TGATAGGCTGTAACCCAACAT-TGTCACCATAAATCACATTGTTAGACTA
PSE	(590)	TGA-ACAAAGGGACTCTA-ATCTGGCAGGAT-ATTC-CA----AAG-C-A
HKLK2.LA0	(7143)	TCCAGTG-TGGCC-CAAGCTCCCGTGTAACACAGGCACTCTAAACAG--
PSE	(638)	T-TAGAGATGACCTCTTGC-AAAG-AAAAAGAAATGGAAAAGAAAAAGAA
HKLK2.LA0	(7189)	-G-CAGGATATTTCAAAAGCTT-AGAGATGACCTCCCAGGAGCTGAATGC
PSE	(677)	AGAAAGGAAAAAAAAAAAAAAAAAGAGATGACCTCTCAGGCTCTGAGGGG
HKLK2.LA0	(7236)	AAA-GACCTGGCCTCTTTGGGCAAGGAGAATCCTTTACCGCACACTCTCC
PSE	(727)	AAACG-CCTGAGGTCTTTGAGCAAGGTCAGTCCTCTGTTGCACAGTCTCC
HKLK2.LA0	(7285)	TTACACAGGGTTATTGTGAGGATCAAATGTGGTCAATGTGTGTGAGACACCA
PSE	(776)	CTCACAGGGTCATTGTGACGATCAAATGTGGTCACGTGTATGAGGCACCA
HKLK2.LA0	(7335)	GCACATGTCTGGCTGTGGAGAGTGAATTCTA--TGTGTGCTAACATTGCT
PSE	(826)	GCACATGCCTGGCTCTGGGGAGTGCCGTGTAAGTGTATGCTTGCACGTCT
HKLK2.LA0	(7383)	GAGTGCTAAGAAAGTATTAGGCAAGGCT-TTCAGCACTCACAGATGCTCA
PSE	(876)	GAATGCTTGGGATGIGTCAGGGAT-TATCTTCAGCACCTACAGATGCTCA

FIGURE 2A

HKLK2.LA0	(7432)	TCTAATCCTCACAAACATGGCTACAGGG-TGGGCACTACTAGCCTCATTTG
PSE	(925)	TCTCATCCTCACAGCATCACTA-TGGGATGGGTATTACTGGCCTCATTTG
HKLK2.LA0	(7481)	ACAGAGGAAAG-GACTGTGGATAAGAAGGGGGTGACCAATAGGTCAGAGT
PSE	(974)	ATGGA-GAAAGTGGCTGTGGCTCAGAAAGGGGGGACCACTAGACCAGGGA
HKLK2.LA0	(7530)	CATTCTGGATGCAAGGGG-CTCCAGAGGACCATGATTAGACATTGTCTGC
PSE	(1023)	CACTCTGGATGC-TGGGGACTCCAGA-GACCATGACCACTACCAACTGC
HKLK2.LA0	(7579)	AGAGAAATT----ATGG-CTGGATGTCTCTGCCCGGAAAGGG-GGA--T
PSE	(1071)	AGAGAAATTAATTGTGGCCT-GATGTCCCTGTCTCTGGAGAGGGTGGAGGT
HKLK2.LA0	(7621)	GCACCTTCCTTGACCCCTATCTCAGATCTTGACTTTGAG-GTTATCTCA
PSE	(1120)	GGACCTTCACTAACCTCCTACCT-TGACCCTCTCTTTTAGGGCTCTTTCT
HKLK2.LA0	(7670)	GACTTCCTCTATGATACCAGGAGCCCATCATAATCTCTCTGTGTCTCTCT
PSE	(1169)	GACCTCCACCATGGTACTAGGA-CCC--CATTGTAT-TCTGT-ACC-CT-
HKLK2.LA0	(7720)	CCCTTCCTCAGTCTTACTG-CCCACTCTTCCCAGCTCCATCTCCAGCTGG
PSE	(1212)	--C-T--TGACTC-TA-TGACCCCACTGCCCA-CTGCA--TCCAGCT--
HKLK2.LA0	(7769)	CCAGGTGTAGCCACAGTACCTAACTCT-TTGCAGAGAACTATAAATGTGT
PSE	(1250)	---GG-GT--CC-C-CT-CCTATCTCTATT-CCCAG--CTGGCCA-GTGC
HKLK2.LA0	(7818)	A-TCCTACAGGGGAGAAAAAAA-AAAAG-AACTCTGAAAGAGCTGACATT
PSE	(1287)	AGT-CT-CAGTGCCCACTGTTTGTGAGTAACCTCTGAAGGGGCTGACATT
HKLK2.LA0	(7865)	TTACCGACTTGCAAAACACATAAGCTAACCTGCCAG--TTTTGT---GCT
PSE	(1335)	TTACTGACTTGCAAAACAAATAAGCTAACCTTCCAGAGTTTGTGAATGCT
HKLK2.LA0	(7909)	GGTAGAACT-CATGAGACICCTGGGTCAGAGGCAAAAGATTTATTACCC
PSE	(1385)	GGCAG-AGTCCATGAGACICCTGAGTCAGAGGCAAAAGGCTTTTACTGCTC

FIGURE 2B

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HKLK2.LA0	(7958)	ACAGCTAAGGAGGCAGCATGAACTTTGTGTTACATTTGTTCACTTTGCC
PSE	(1434)	ACAGCTTAGCAGACAGCATGAGGTTTCATGTTACATTAGTACACCTTGCC
HKLK2.LA0	(8008)	CCCC--AATTCATAT-GGGATGATCAGAGCAGTTC-AGGTGGATG--G-A
PSE	(1484)	CCCCCAAATCTTGTAGGG-TGACCAGAGCAG-TCTAGGTGGATGCTGTG
HKLK2.LA0	(8051)	CA-CAGGGGTTTGTGGCAAAGGTGAGCAACCTAG-GCTTAGAAATCCTCA
PSE	(1532)	CAGAAGGGGTTTGTGCCACTGGTGAGAAACCT-GAGATTAGGAATCCTCA
HKLK2.LA0	(8099)	ATCTTATAAGAAGGTACT---AGCAAACCTTGTC-CAGTCTTTGTATCTGA
PSE	(1581)	ATCTTAT-ACTGGG-ACAACCTGCAAACCTG-CTCAGCCTTTGTCTCTGA
HKLK2.LA0	(8145)	CGGAGATATTATCTTTATAAT-TGGG-TTGAAAGCAGACCTACTCTGGAG
PSE	(1628)	TGAAGATATTATCTTCATGATCTTGGATTGAAAACAGACCTACTCTGGAG
HKLK2.LA0	(8193)	GAACATATTGTATTTATTGTCCT-GAACAGTAAACAAATCTGCTGTAAAA
PSE	(1678)	GAACATATTGTATCGATTGTCCTTG-ACAGTAAACAAATCTGTTGT--AA
HKLK2.LA0	(8242)	TAGACGTAACTTTATTATCTAAGG-CAGTAAGCAAACCTAGATCTGAAG
PSE	(1725)	GAGACATTATCTTTATTATCT-AGGACAGTAAGCAAGCCTGGATCTG-AG
HKLK2.LA0	(8291)	-GCGATACCATCTTGCAAGGCTATCTGCTGTACAAATATGCTTGAAAAGA
PSE	(1773)	AGAGATATCATCTTGCAAGGATGCCTGCTTTACAAACATCCTTGAAACAA
HKLK2.LA0	(8340)	TGGTCCAGAAAAGAAAACGGTATTATTGCCTTTGCTCAGAAGACACACAG
PSE	(1823)	CAATCCAGAAAA-AAAAAGGTTGCTGTCTTTGCTCAGAAGACACACAG
HKLK2.LA0	(8390)	AAACATAAGAGAACCATGGAAAATTGTCTCCCAACACTGTTACCCAGAG
PSE	(1872)	ATACGTGACAGAACCATGGAGAATTGCCTCCCAACGCTGTTACGCCAGAG
HKLK2.LA0	(8440)	CCTTCCACTCTTGTCTGAGGACAGTCTTAAACATCCCAICATTAAG-T-GT
PSE	(1922)	CCTTCCACCTTGTCTGAGGACAGTCTTAAACGTTCCACCATTAATACT

FIGURE 2C

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HKLK2.LA0	(8488)	--GTCTACCACATCTGGCTTCACCGTGCCTAACCAAGATTTCTAGGTCCA
PSE	(1972)	TCTTCTATCACATCCTGCTTCTTTATGCCTAACCAAG-GTTCTAGGTCCC
HKLK2.LA0	(8536)	GTTCCCCACCATGTTTGGCAGTCCCCCACTGCCAACCCCAGAATAAGGGA
PSE	(2021)	GAT--CGACTG1GTCTGGCAGCACTCCACTGCCAAACCCAGAATAAGGCA
HKLK2.LA0	(8586)	GTGCTCAGAATTCCGA
PSE	(2069)	GCGCTCAGGATCCCGA

FIGURE 2D

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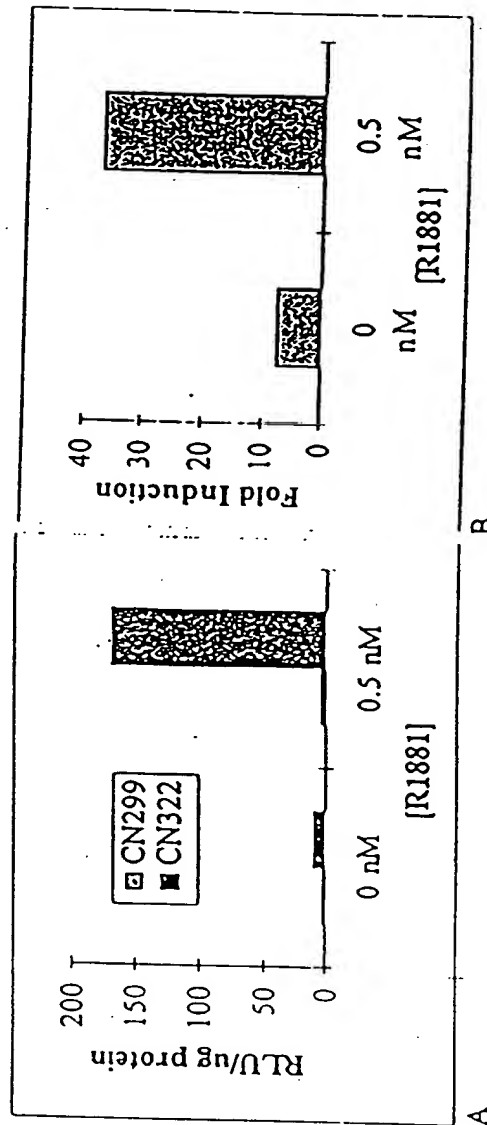


FIGURE 3

FO2201-8225/860

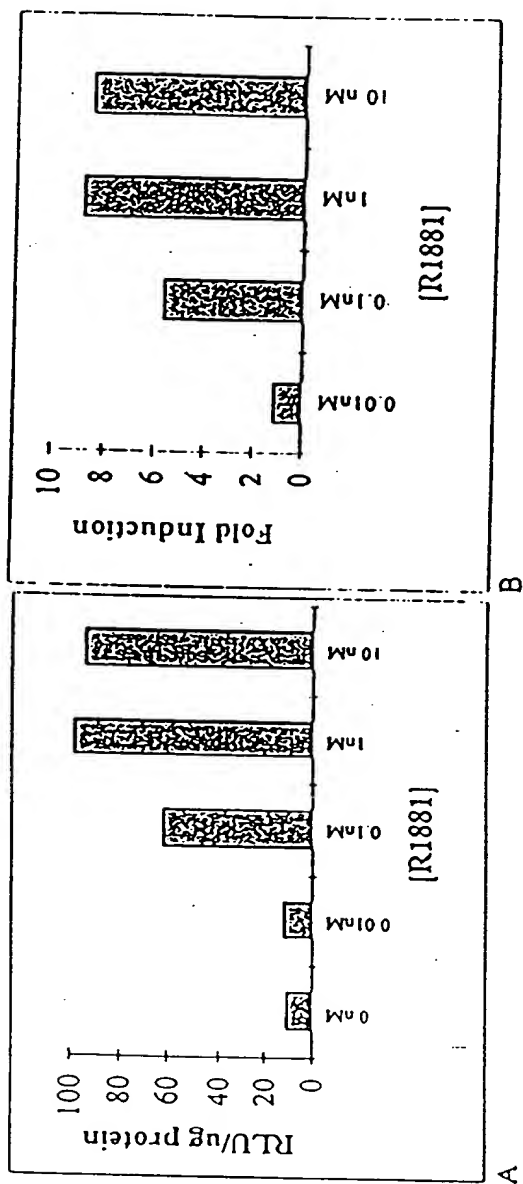


FIGURE 4

FOOT: 82252860

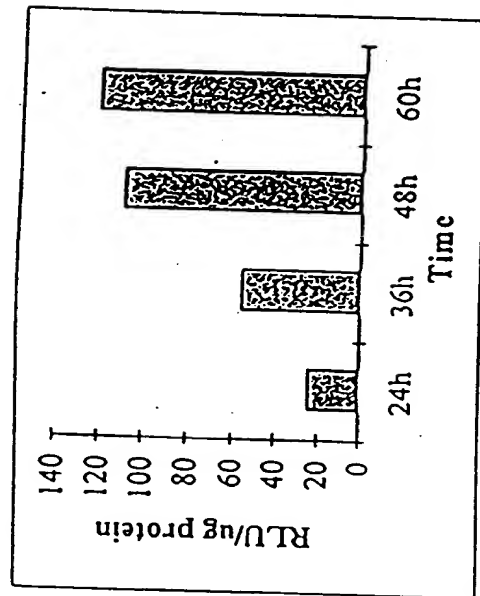


FIGURE 5

FOI220T-82252860

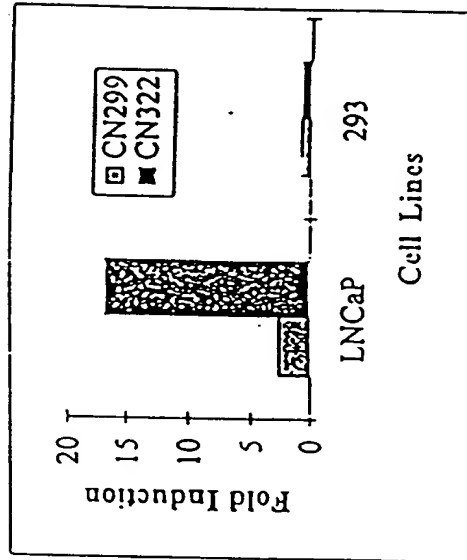


FIGURE 6

FOOT-82252860

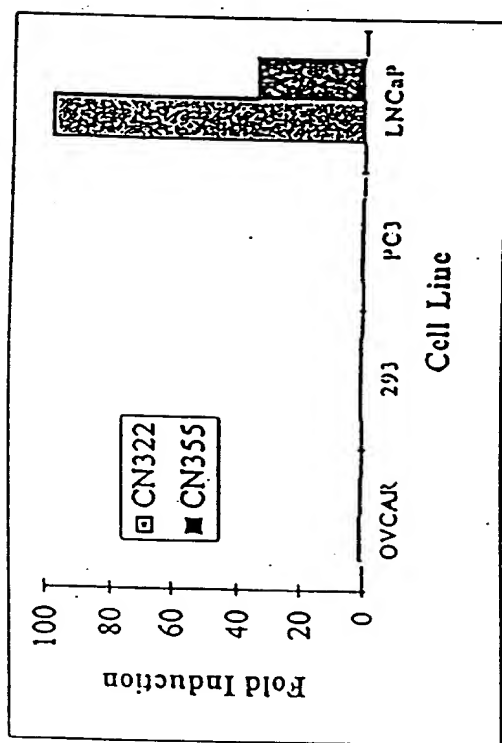


FIGURE 7

09875228.1

			Fold Induction
CN379	-5155	-3387	-324
			81
CN386		-3529	
			50
CN387		-3643	
			90
CN388	-4814	-3387	
			35
CN389		-3529	
			30
CN390		-3643	
			96
CN391	-4457	-3387	
			61
CN392		-3529	
			53
CN393		-3643	
			30
CN394		-3993	-3387
			55
CN395		-3529	
			45
CN396		-3643	
			37

FIGURE 8

0965257860

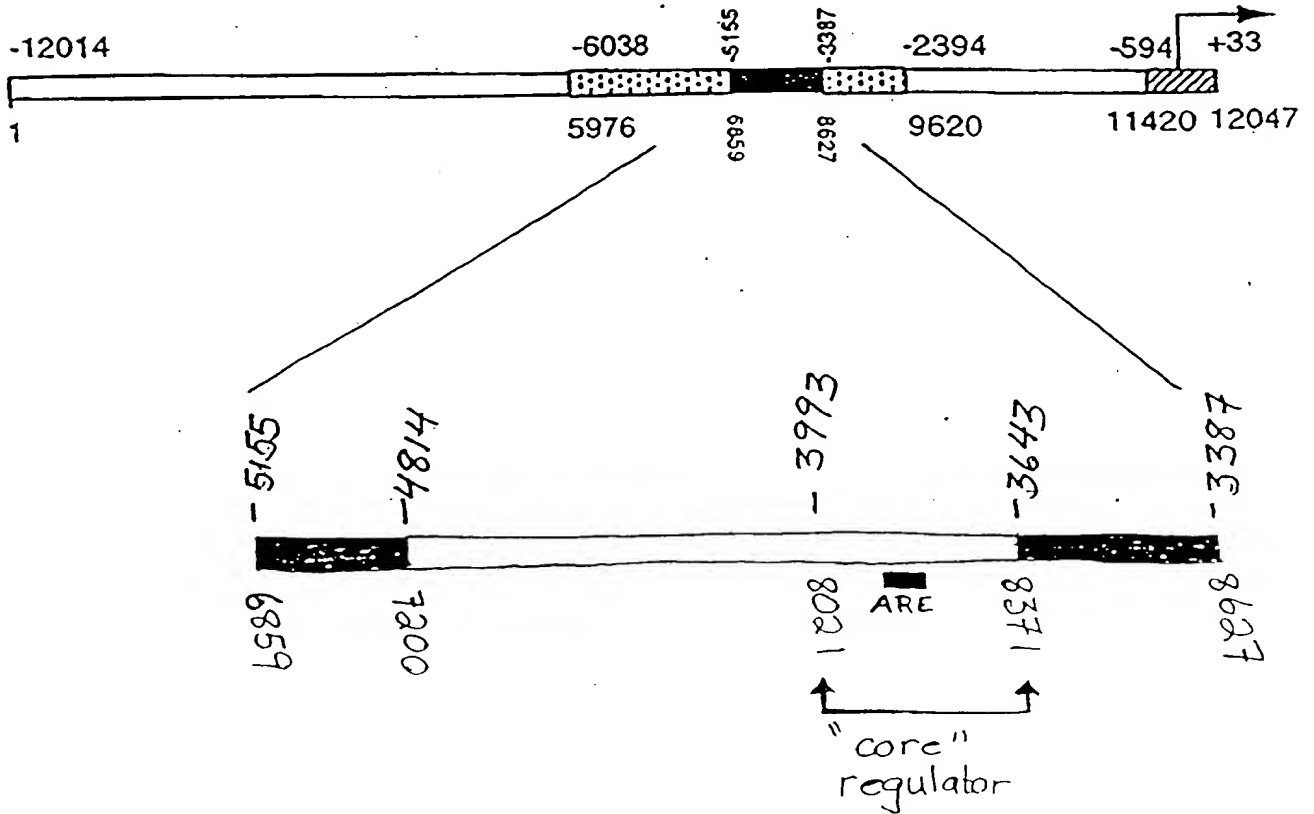
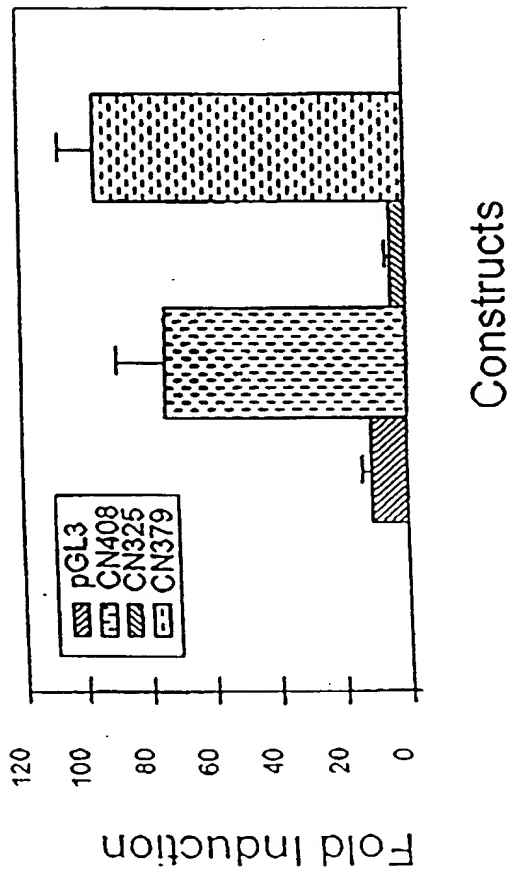


FIGURE 9

A



B

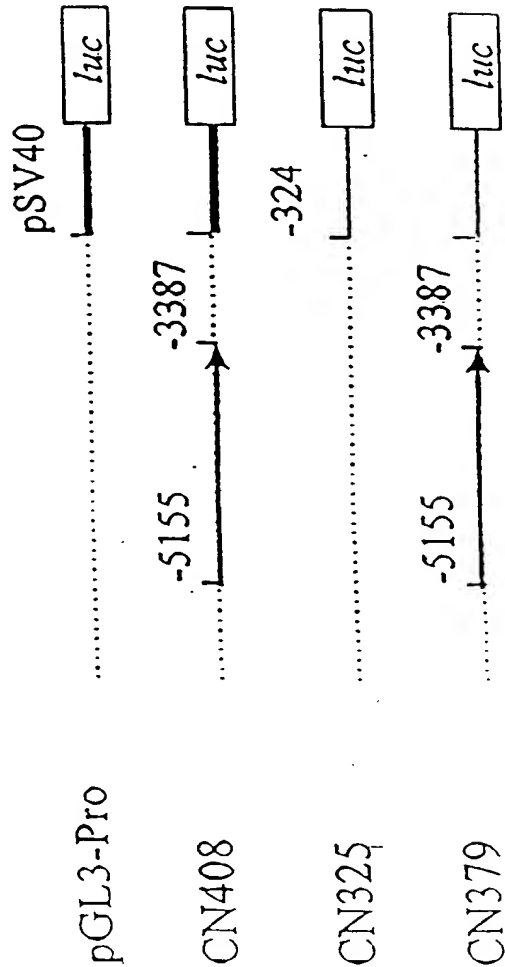


FIGURE 10

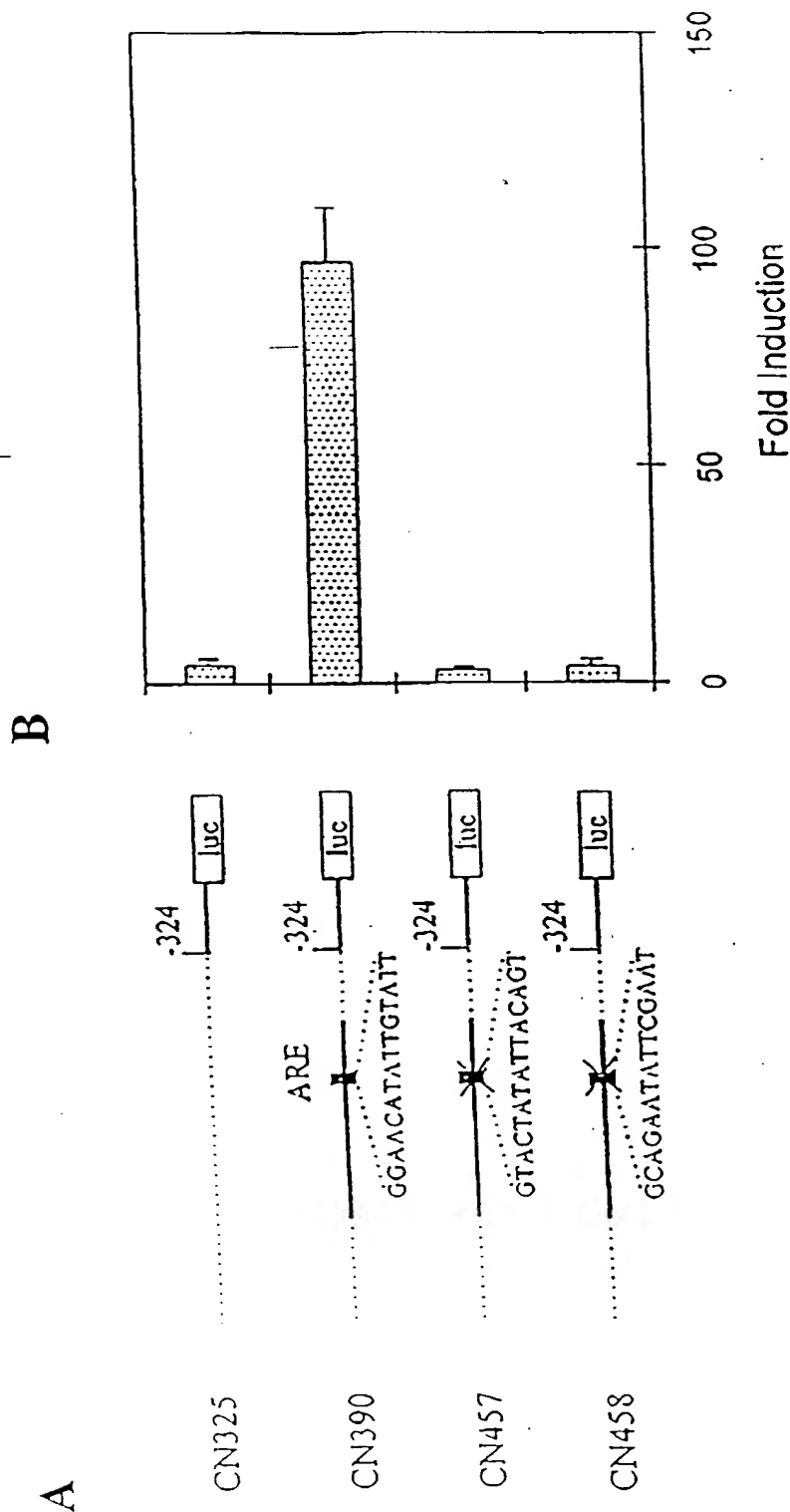


FIGURE 11

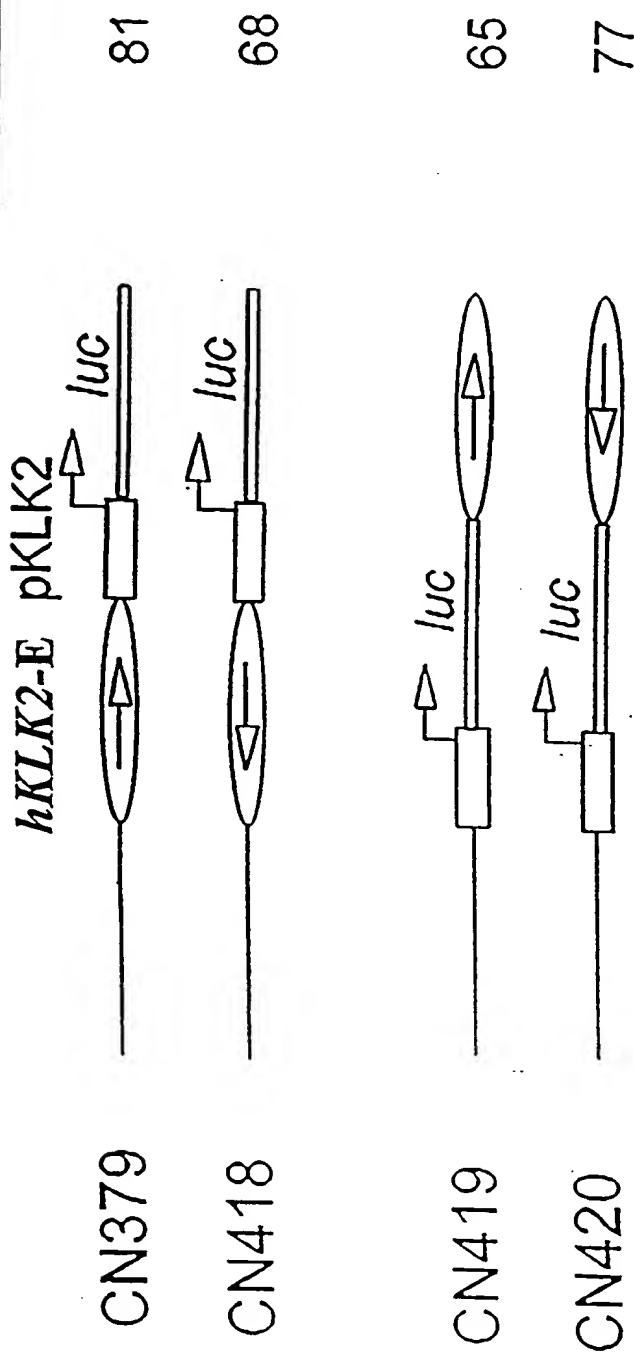
Fold Induction

FIGURE 12

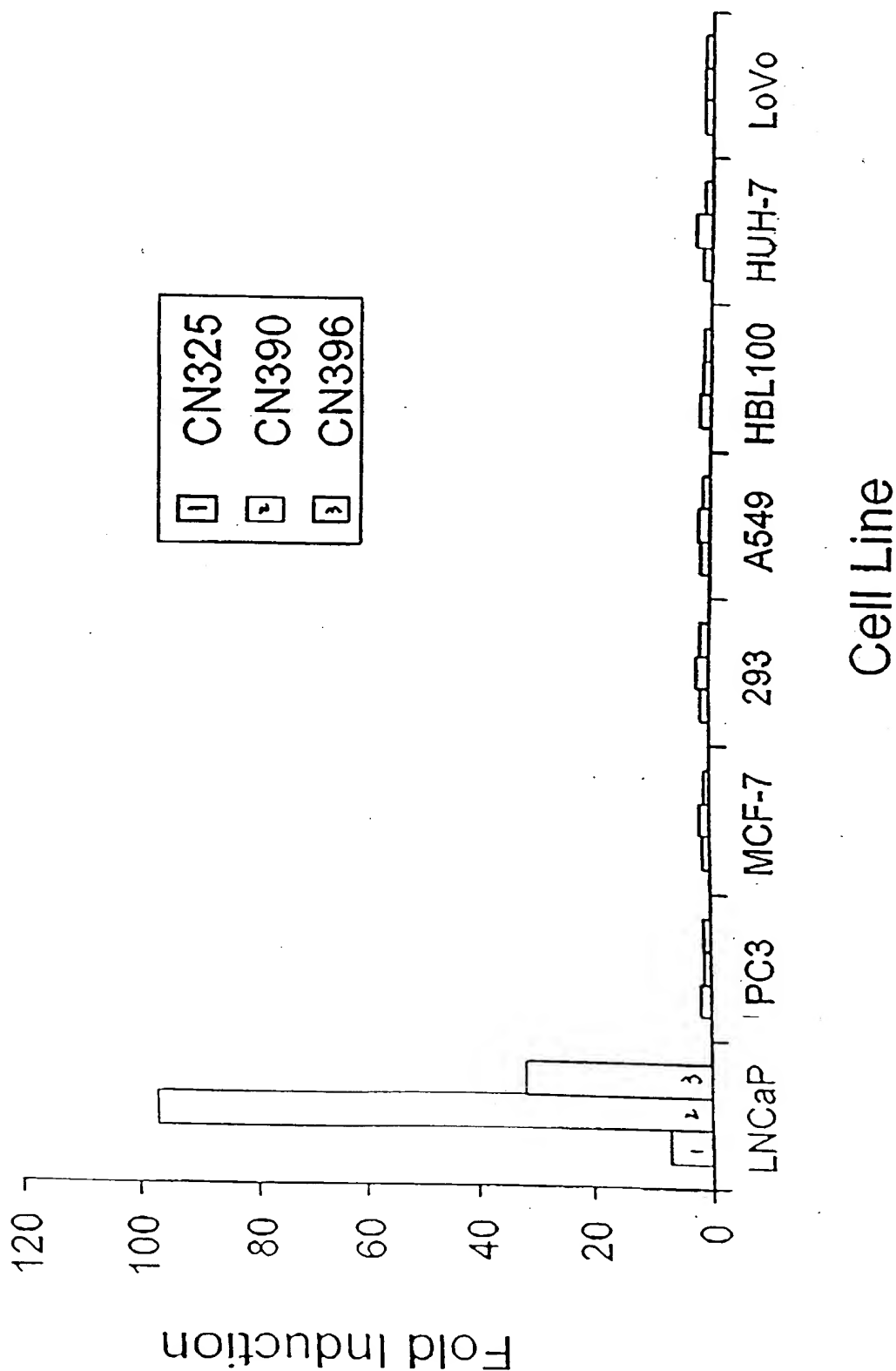


FIGURE 13

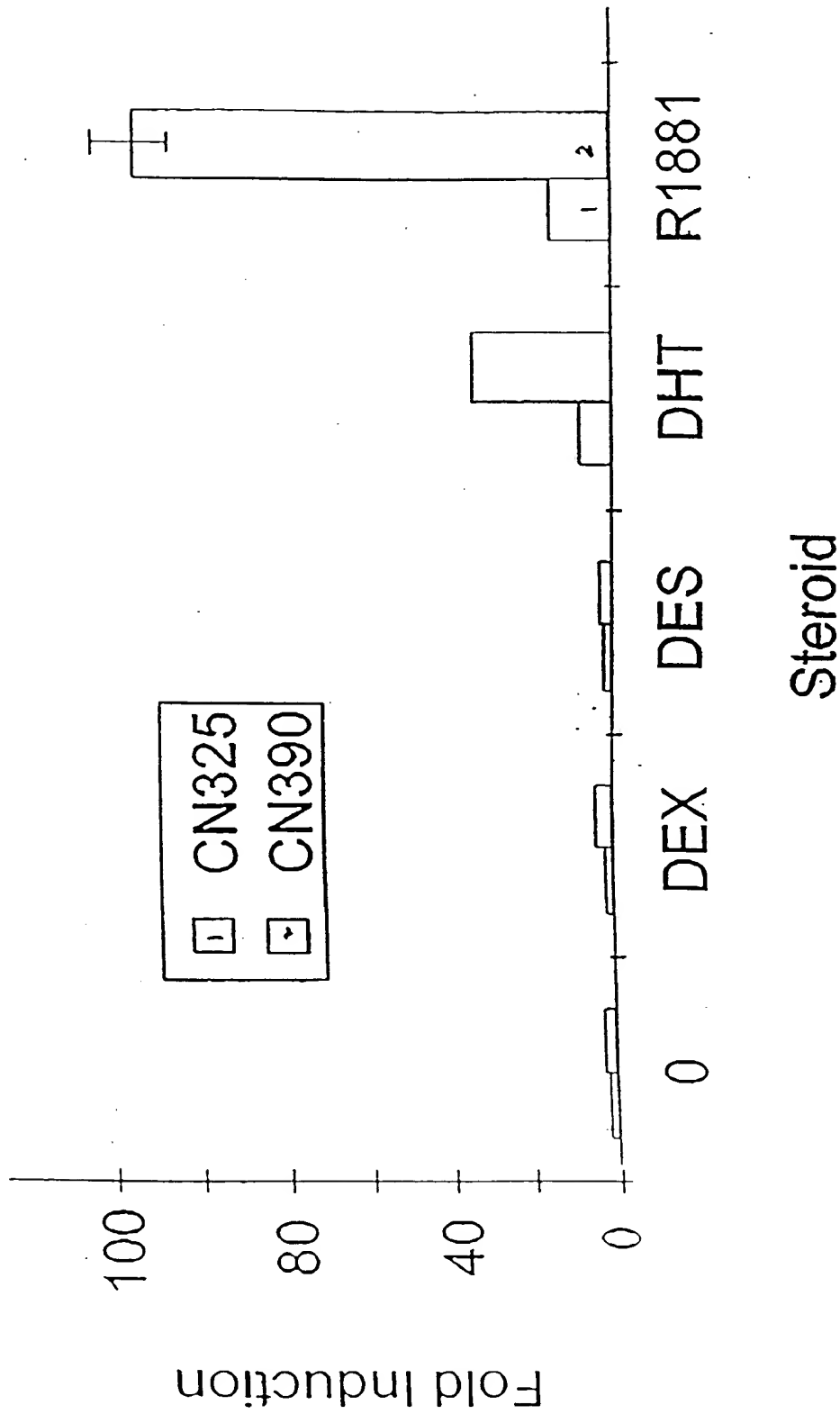


FIGURE 14

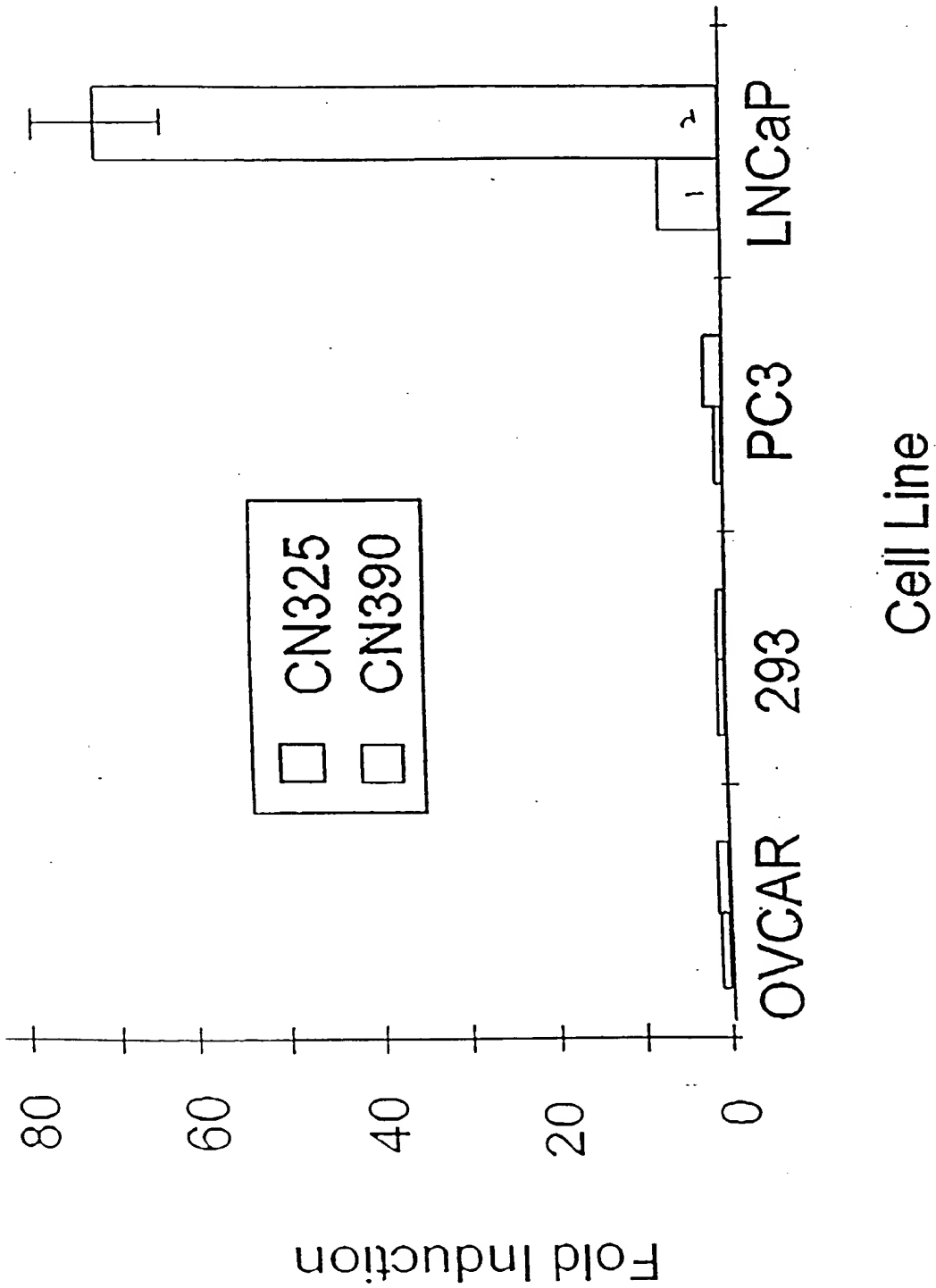


FIGURE 15

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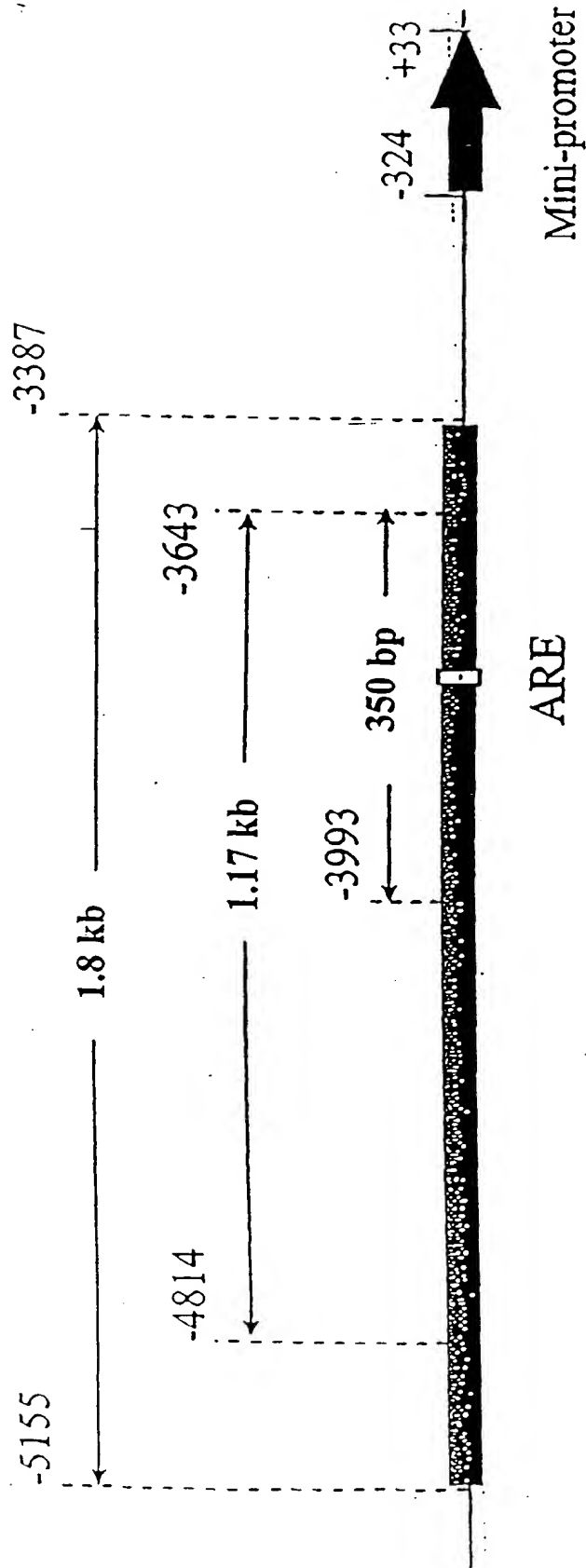


FIGURE 16

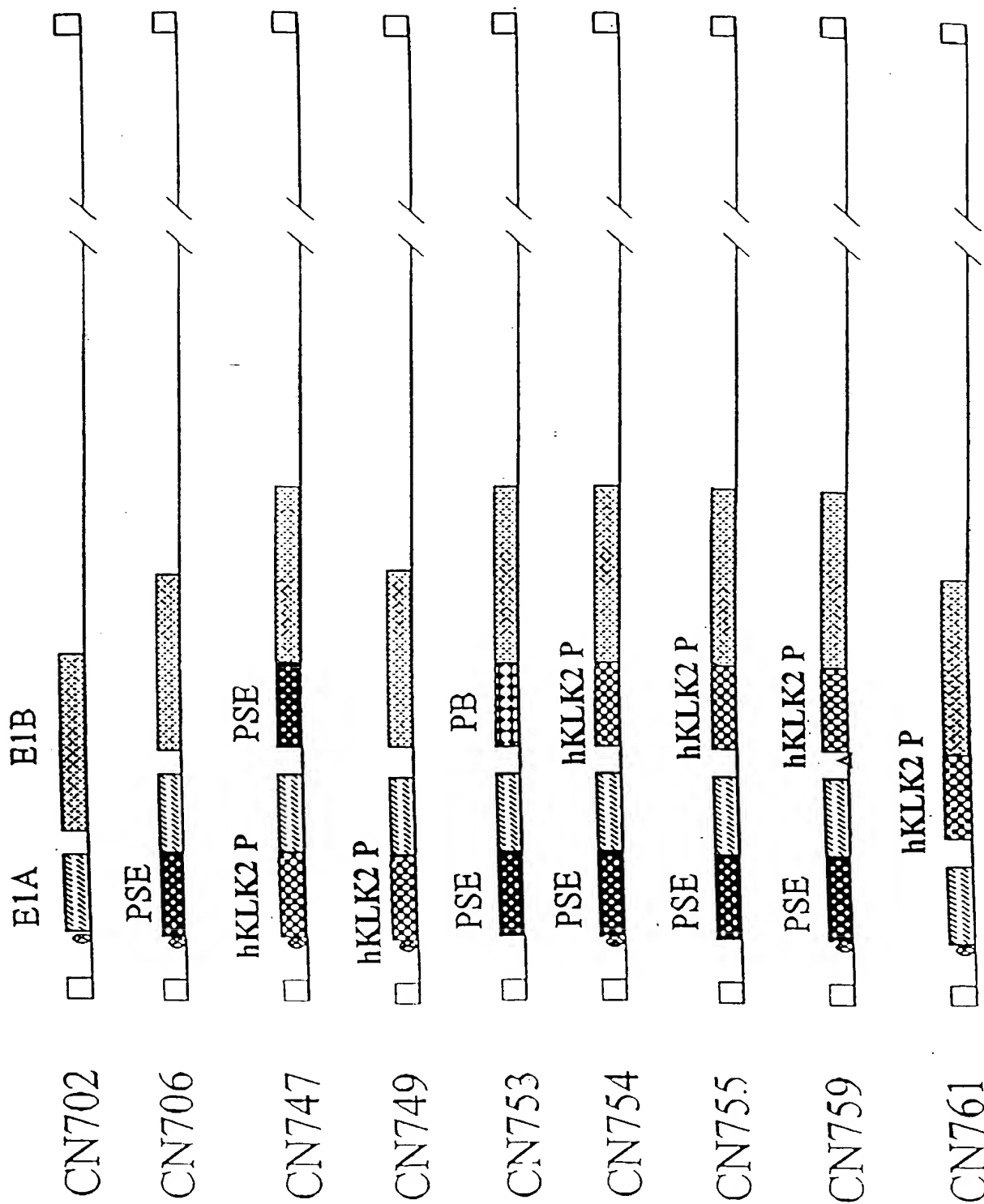
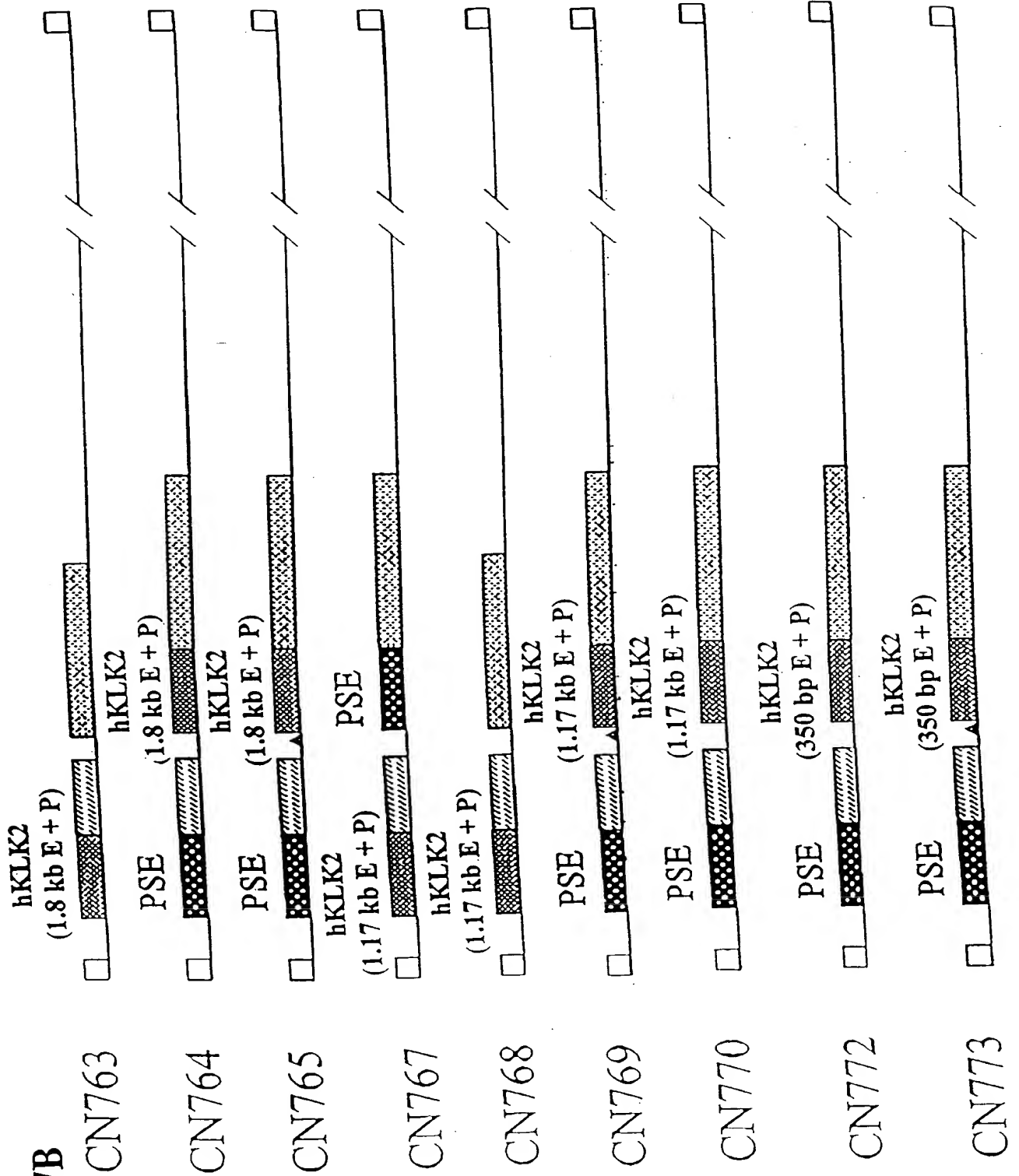


FIGURE 17A

FIGURE 17B



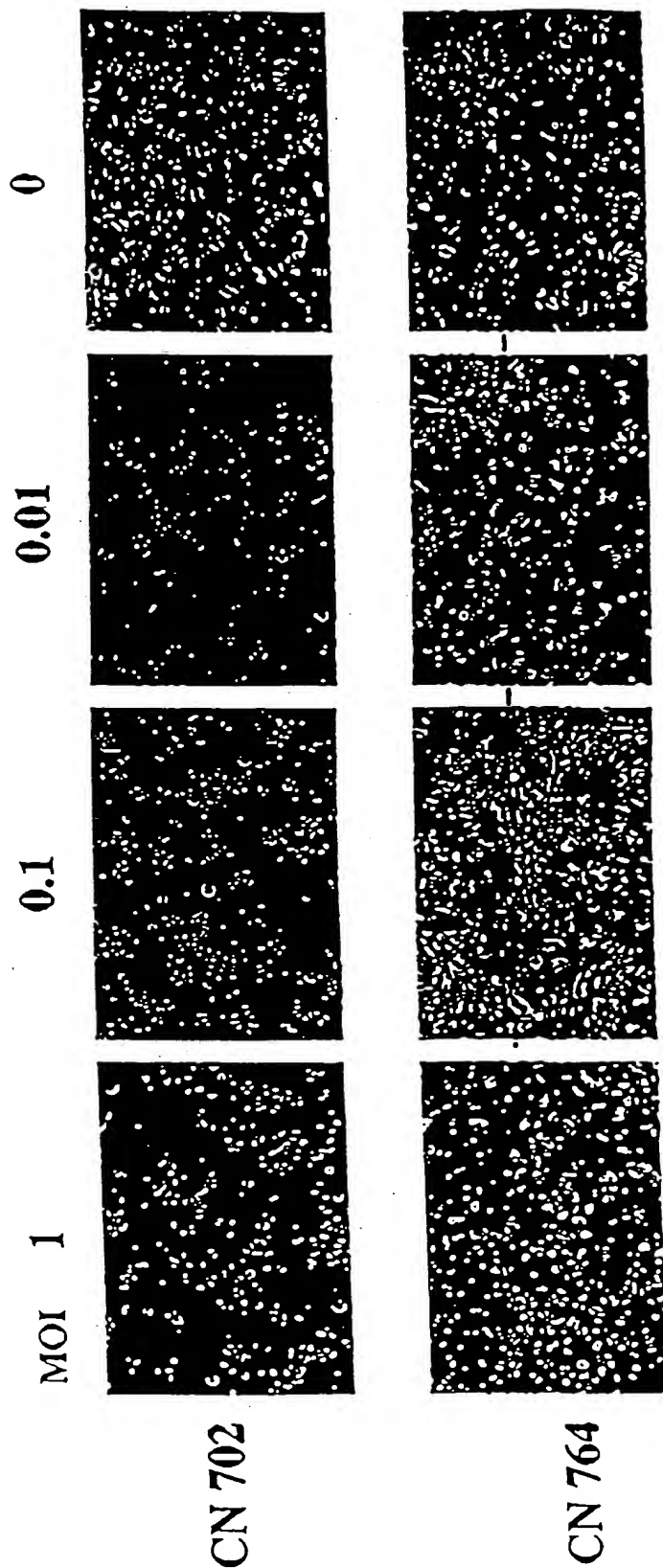


FIGURE 18

FOOT-82254860

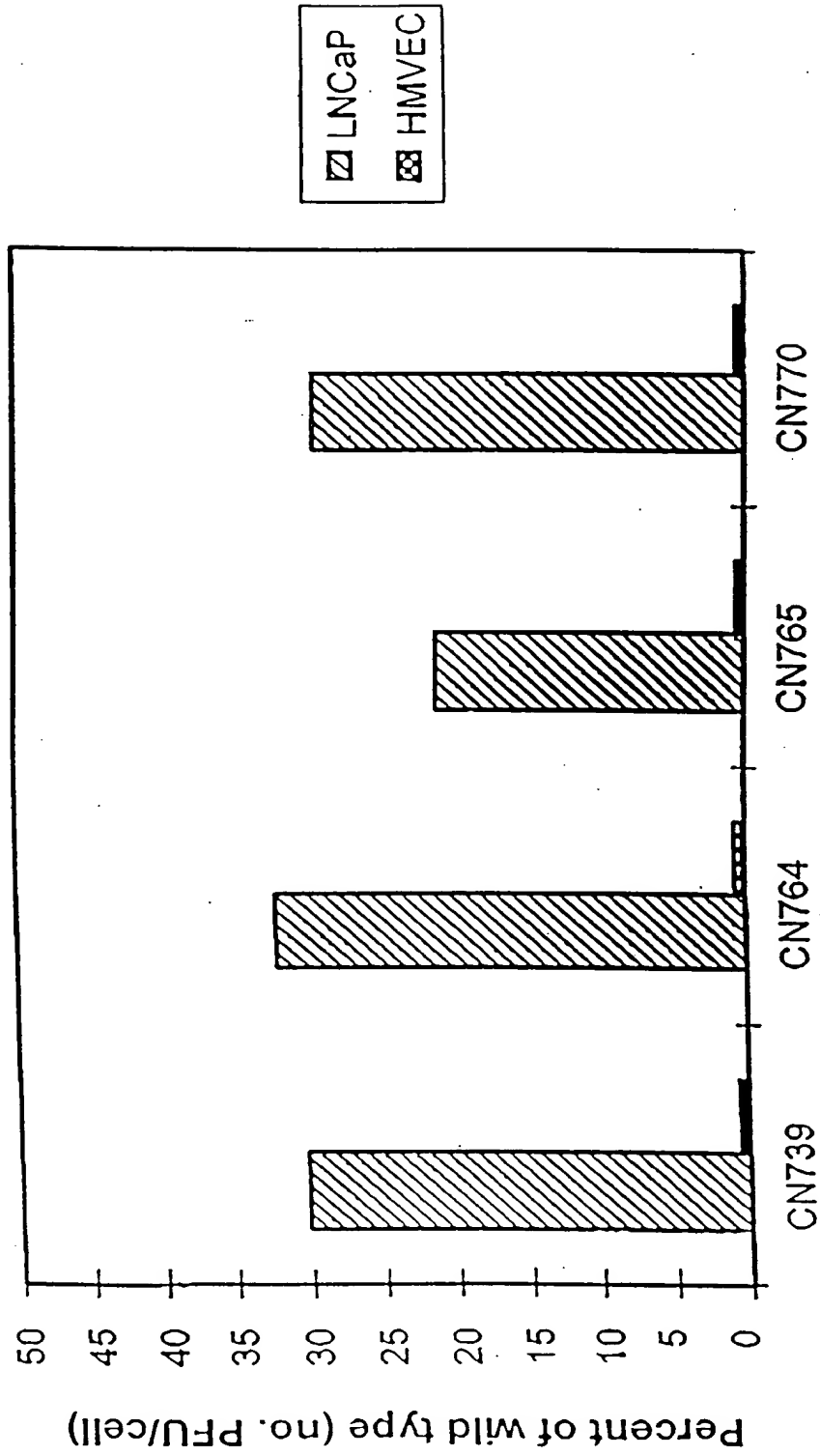


FIGURE 19

FIGURE 19

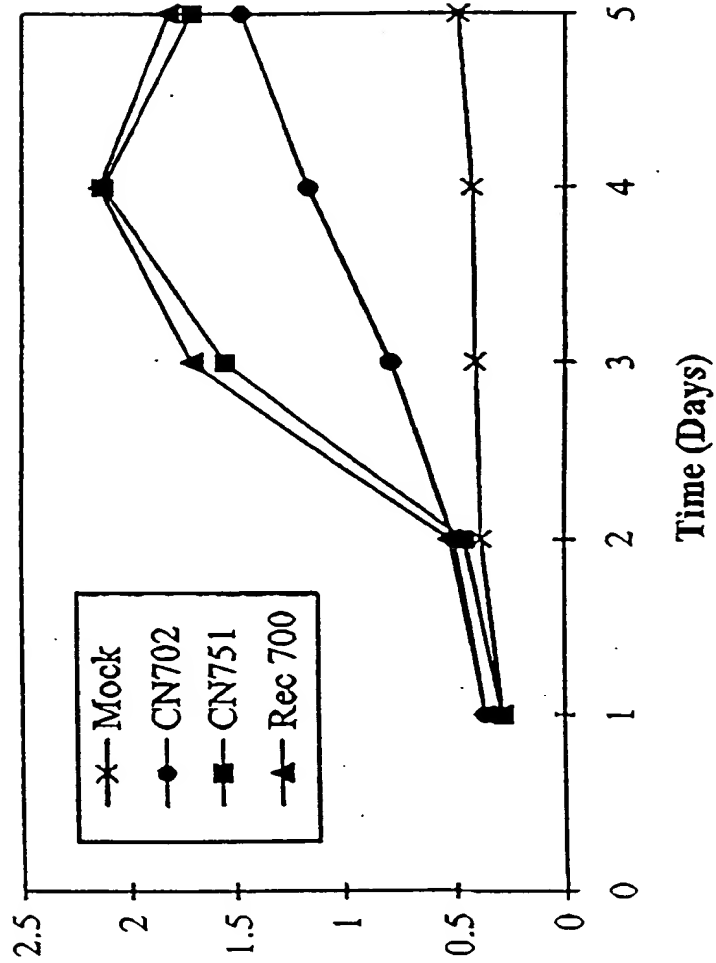


FIGURE 20

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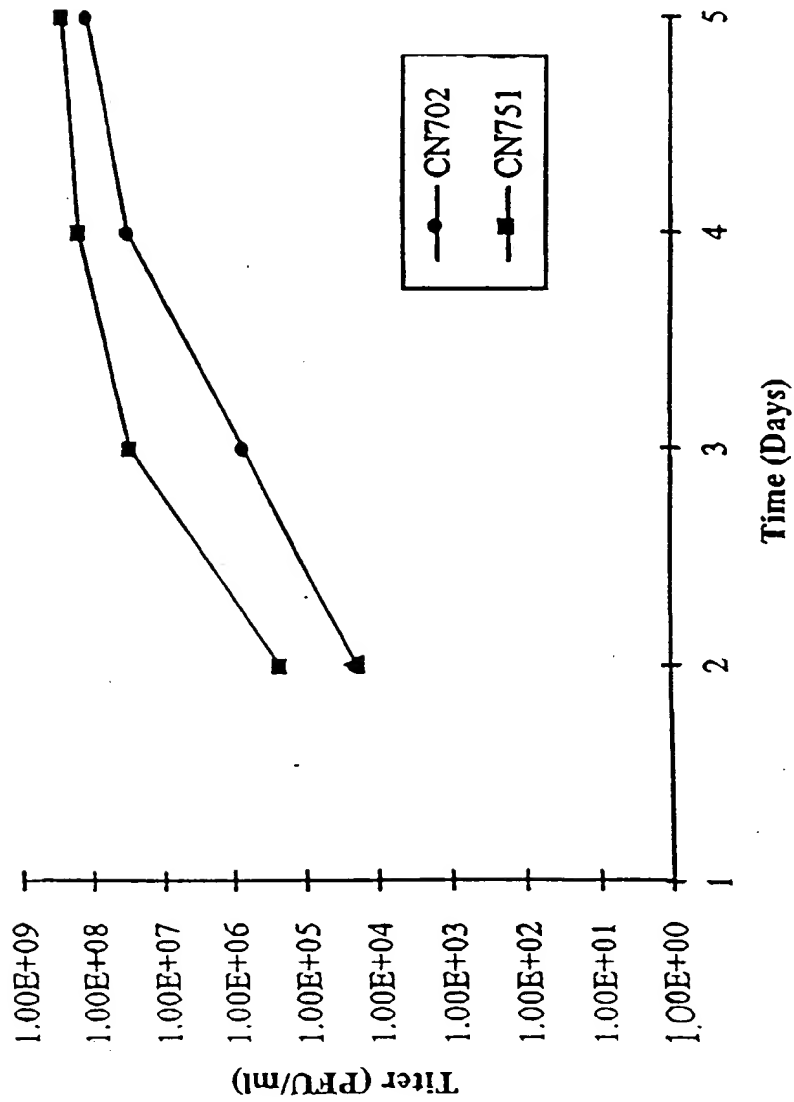


FIGURE 21

FO220T" 82254960

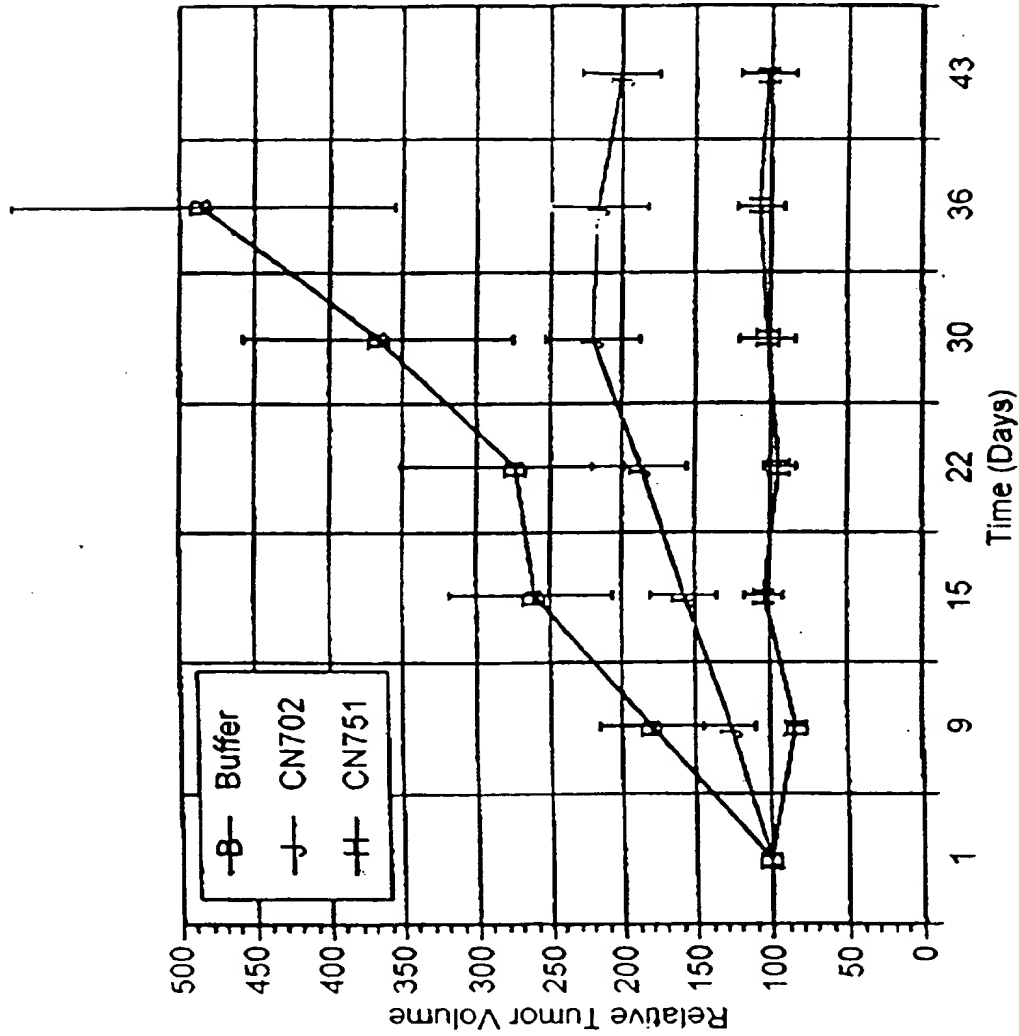


FIGURE 22

FIGURE 22

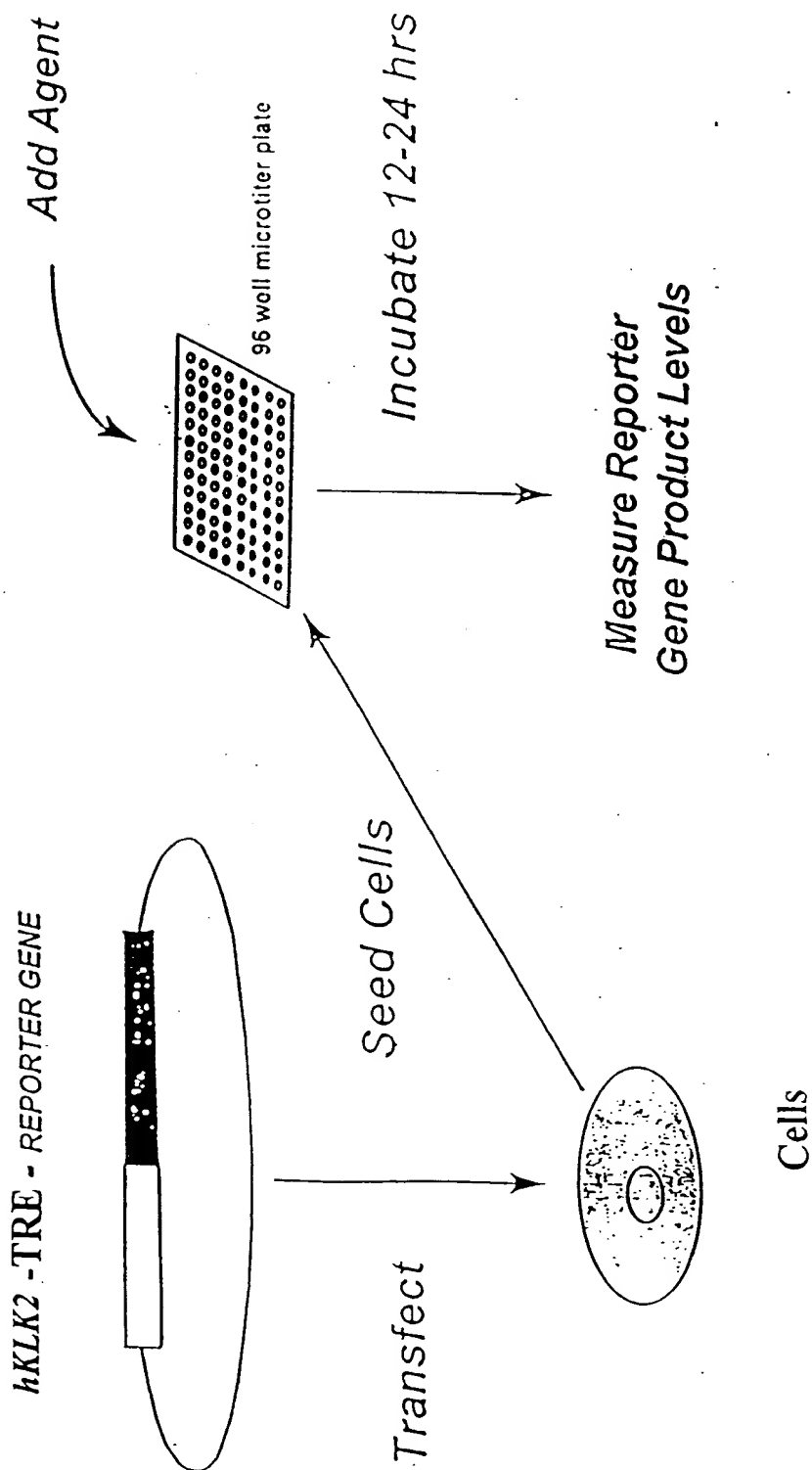


FIGURE 23A

102201" 82254860

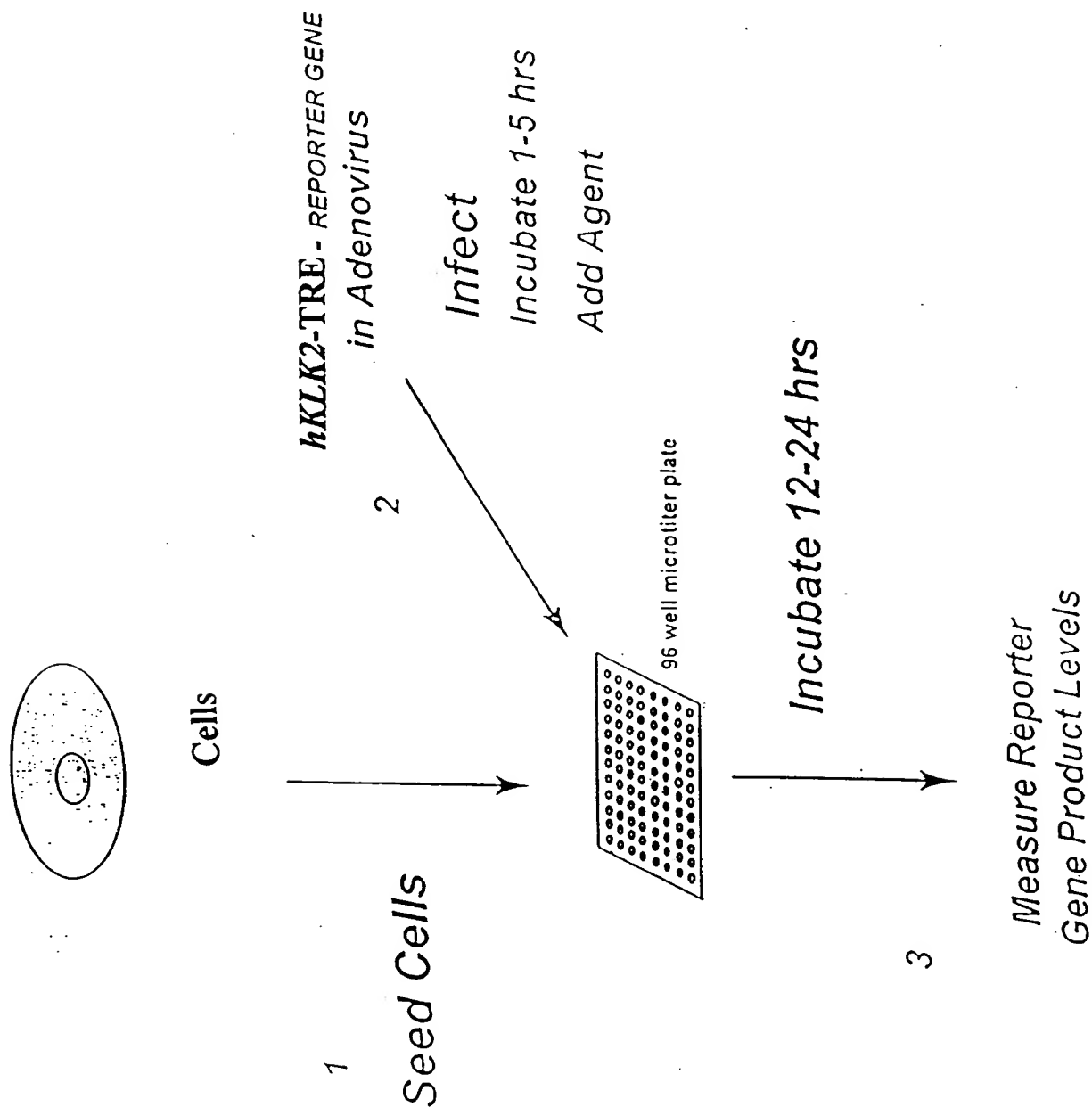


FIGURE 23B

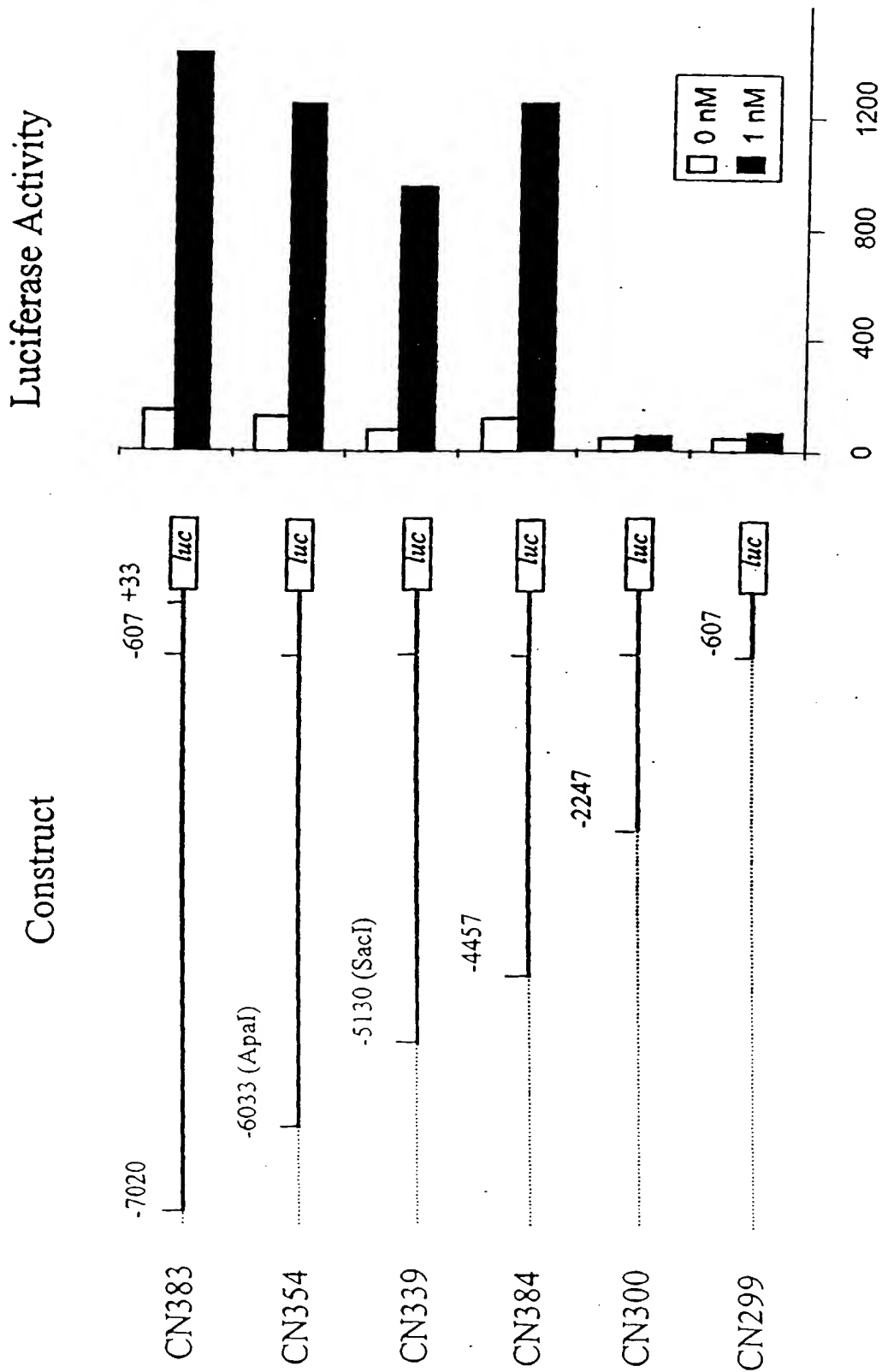
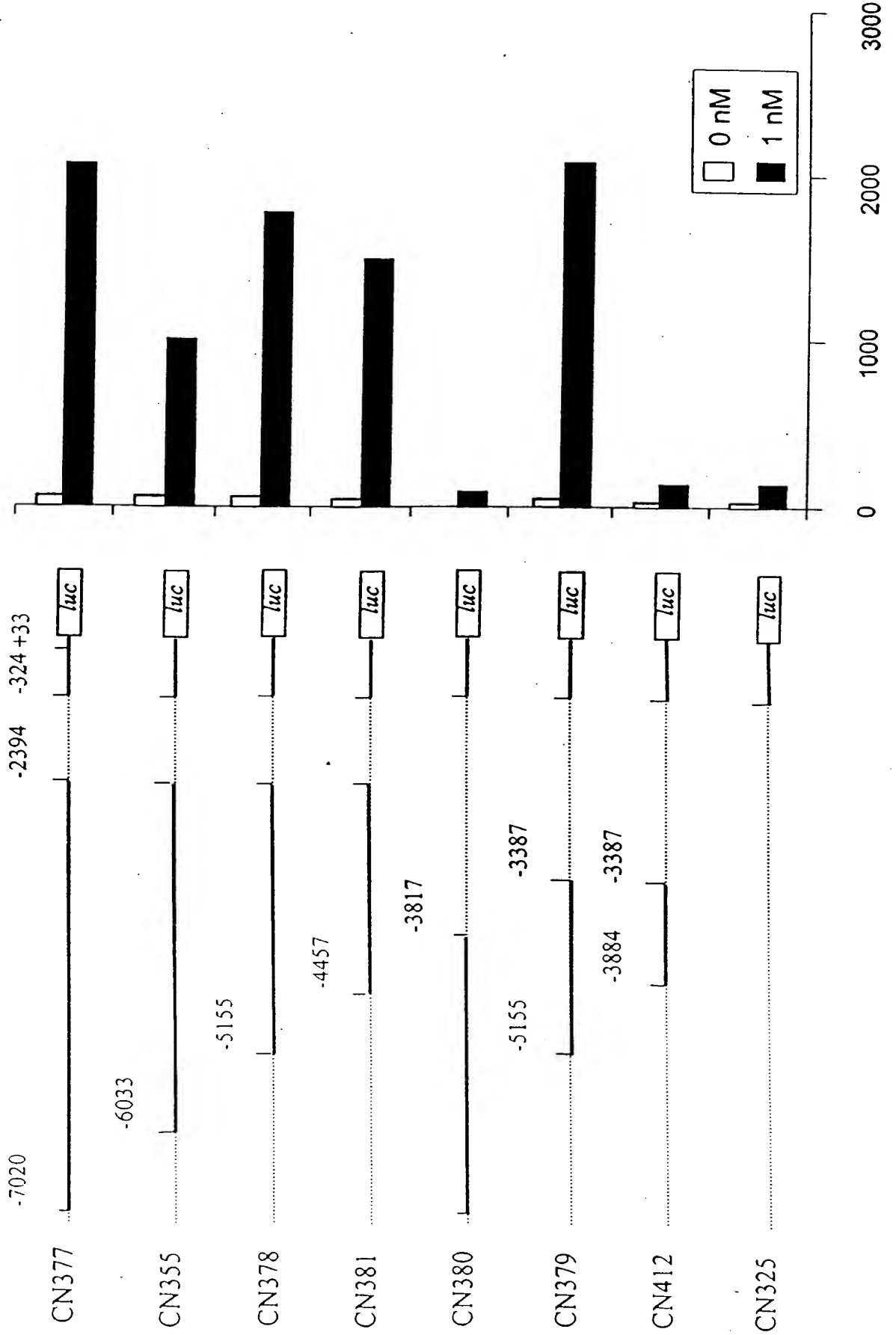


FIGURE 24A

FIGURE 24B

Construct

Luciferase Activity



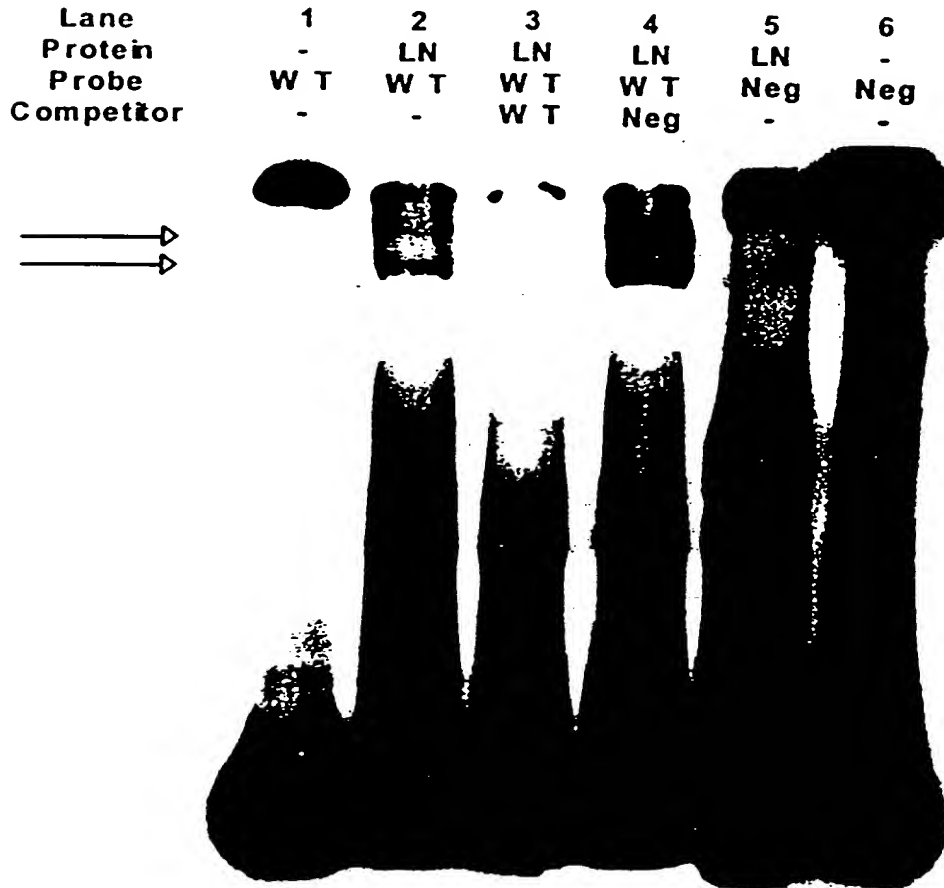


FIGURE 25A

09875228-102201

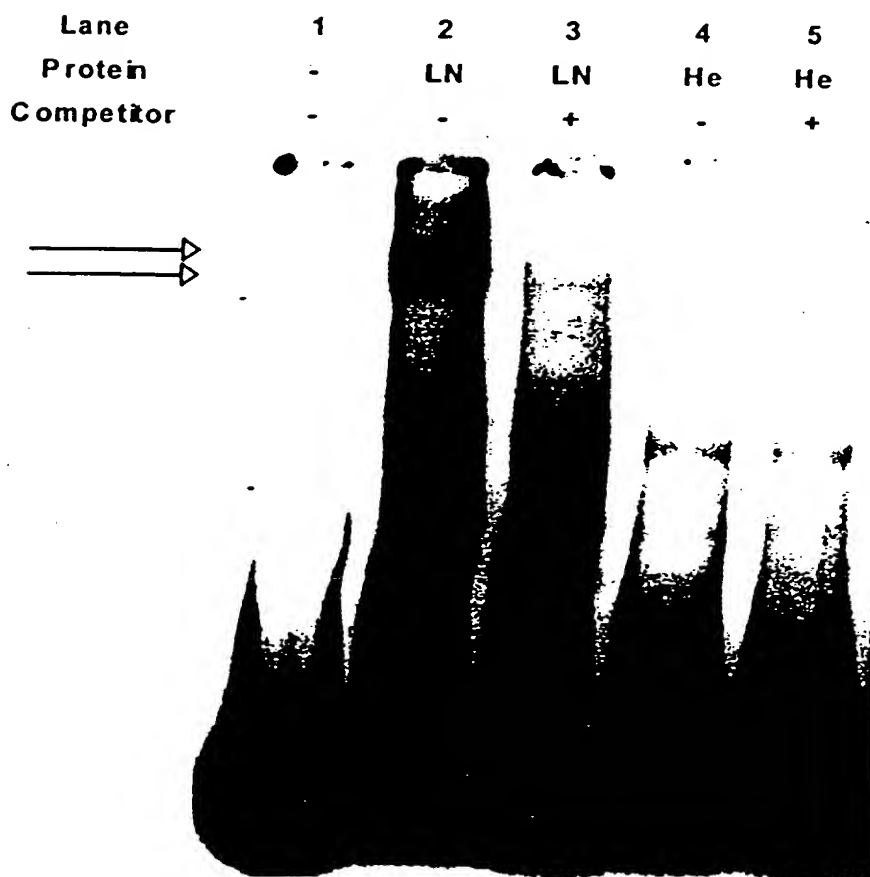


FIGURE 25B

09875228-102201

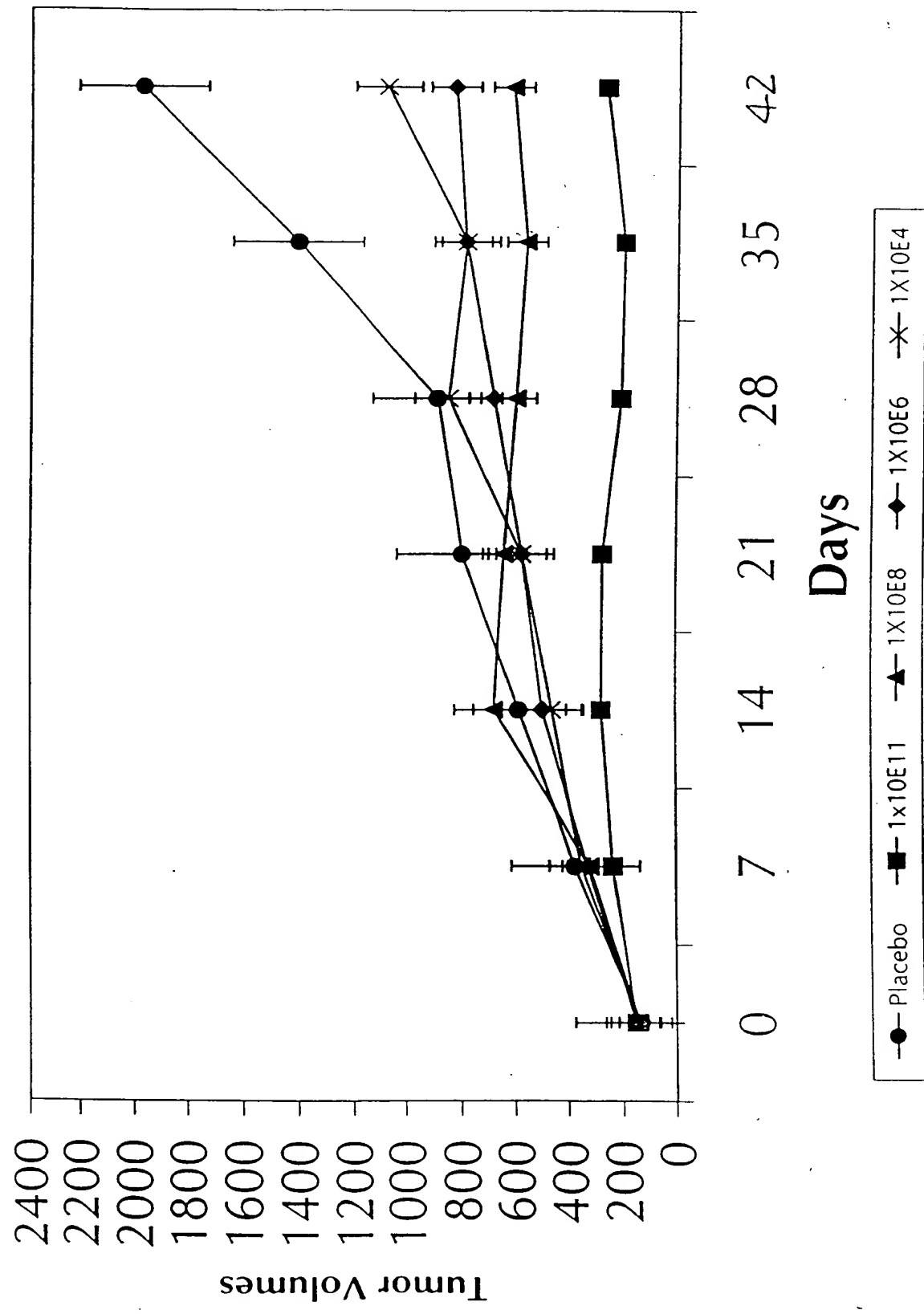


FIGURE 26

FIGURE 26